

AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claims 1-171 (cancelled)

Claim 172 (withdrawn) A method of feeding an animal comprising feeding the animal a corn grain obtained from a transgenic corn plant comprising in its genome a chimeric gene selected from the group consisting of:

(i) a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-9 stearyl ACP desaturase consisting essentially of the amino acid sequence set forth in SEQ ID NO:9, wherein all or a part of the isolated nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-9 stearyl ACP desaturase, or the complement of all or a part of the isolated nucleic acid fragment, operably linked to at least one regulatory sequence;

(ii) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-9 stearyl ACP desaturase consisting essentially of the amino acid sequence set forth in SEQ ID NO:9, wherein all or a part of the isolated nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-9 stearyl ACP desaturase, or the complement of all or a part of the isolated nucleic acid sequence and (b) an isolated nucleic acid fragment comprising a corn oleosin promoter consisting essentially of the nucleotide sequence set forth in any of SEQ ID NOS: 38-40 and 42-49, wherein the isolated nucleic acid fragments of (a) and (b) are operably linked;

(iii) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-9 stearyl ACP desaturase consisting essentially of the amino acid sequence set forth in SEQ ID NO:9, wherein all or a part of the isolated nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-9 stearyl ACP desaturase, or the complement of all or a part of the isolated nucleic acid fragment and (b) a shrunken 1 intron/exon, wherein the isolated nucleic acid fragments of (a) and (b) are operably linked to at least one regulatory sequence; or

(iv) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-9 stearyl ACP desaturase consisting essentially of the amino acid sequence set forth in SEQ ID NO:9, wherein all or a part of the isolated nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-9 stearyl ACP desaturase, or the complement of all or a part of the isolated nucleic acid fragment (b) an isolated nucleic acid fragment comprising a corn oleosin promoter consisting essentially of the amino acid sequence set forth in any of SEQ ID NOS: 38-40 and 42-49, and (c) a shrunken 1 intron/exon, wherein (a), (b) and (c) are operably linked;

and further wherein expression of the chimeric gene results in an altered corn stearic acid phenotype.

Claims 173 (withdrawn) A method feeding an animal comprising feeding the animal a corn grain obtained from a transgenic corn plant comprising in its genome a chimeric gene selected from the group consisting of:

(i) a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 90% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NO:1, wherein all or a part of the isolated nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-12 desaturase, or the complement of all or part of the fragment, operably linked to at least one regulatory sequence;

(ii) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 90% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NO:1, wherein all or a part of the isolated nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-12 desaturase, or the complement of all or a part of the fragment and (b) an isolated nucleic acid fragment comprising a corn oleosin promoter consisting essentially of the nucleotide sequence set forth in any of SEQ ID NOS: 38-40 and 42-49 wherein the isolated nucleic acid fragments of (a) and (b) are operably linked;

(iii) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 90% based on the Clustal method of alignment when compared to

a nucleic acid as set forth in SEQ ID NO:1, wherein all or a part of the isolated nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-12 desaturase, or the complement of all or a part of the fragment, and (b) a shrunken 1 intron/exon, wherein the isolated nucleic acid fragments of (a) and (b) are operably linked to at least one regulatory sequence; or

(iv) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 90% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NO:1, wherein all or a part of the isolated nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-12 desaturase or the complement of all or a part of the fragment, (b) an isolated nucleic acid fragment comprising a corn oleosin promoter consisting essentially of the nucleotide sequence set forth in any of SEQ ID NOS: 38-40 and 42-49, and (c) a shrunken 1 intron/exon, wherein (a), (b) and (c) are operably linked;

and further wherein expression of the chimeric gene results in an altered corn oleic acid phenotype.

Claim 174 (currently amended) A method of feeding an animal comprising feeding the animal a corn grain obtained from a transgenic corn plant comprising in its genome a chimeric gene selected from the group consisting of:

(i) a first chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-9 stearyl ACP desaturase ~~consisting essentially of~~ comprising the amino acid sequence set forth SEQ ID NO:9 wherein all or a part of the first isolated nucleic acid is useful in co-suppressing an endogenous gene encoding a corn delta-9 stearyl ACP desaturase, or the complement of ~~all or a part of the first fragment thereof~~, and linked to a second chimeric gene comprising a second isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said second fragment has a nucleic acid sequence identity of at least 90% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NO:1, wherein all or a part of the isolated second nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-12 desaturase, or the complement of ~~all or a part of the second fragment thereof~~ thereof, operably linked to at least one regulatory sequence;

(ii) a chimeric gene comprising (a) a first isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase ~~consisting essentially of~~ comprising the amino acid sequence set forth in SEQ ID NO:9 wherein all or a part of the isolated first nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-9 stearoyl ACP desaturase, or the complement of ~~all or a part of the first fragment thereof~~, (b) a second isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said second fragment has a nucleic acid sequence identity of at least 90% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NO:1, wherein all or a part of the isolated second nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-12 desaturase, or the complement of ~~all or a part of the second fragment thereof~~, and (c) a third isolated nucleic acid fragment comprising a corn oleosin promoter ~~consisting essentially of~~ comprising the nucleotide sequence set forth in any of SEQ ID NOS: 38-40 and 42-49 wherein the isolated nucleic acid fragments of (a), (b) and (c) are operably linked;

(iii) a chimeric gene comprising (a) a first isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase ~~consisting essentially of~~ comprising the amino acid sequence set forth in SEQ ID NO:9 wherein all or a part of the isolated first nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-9 stearoyl ACP desaturase, or the complement of ~~all or a part of the first fragment thereof~~, (b) a second isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said second fragment has a nucleic acid sequence identity of at least 90% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NO:1, wherein all or a part of the isolated second nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-12 desaturase, or the complement of ~~all or a part of the second fragment thereof~~, and (c) a shrunken 1 intron/exon, operably linked to at least one regulatory sequence wherein (a), (b) and (c) are operably linked; or

(iv) a chimeric gene comprising (a) a first isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase ~~consisting essentially of~~ comprising the amino acid sequence set forth in SEQ ID NO:9, or the complement thereof, (b) a second isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein

said second fragment has a nucleic acid sequence identity of at least 90% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NO:1, or the complement thereof, (c) a third isolated nucleic acid fragment comprising a corn oleosin promoter ~~consisting essentially of~~ comprising the nucleotide sequence set forth in any of SEQ ID NOS: 38-40 and 42-49, and (d) a shrunken 1 intron/exon wherein (a), (b), (c) and (d) are operably linked;

and further wherein expression of the chimeric gene results in an altered corn oil phenotype compared to the oil phenotype of a non transgenic corn grain.

Claim 175 (cancelled)

Claim 176 (currently amended) A method of feeding an animal comprising feeding the animal a corn grain obtained from a transgenic corn plant comprising in its genome a chimeric gene selected from the group consisting of :

(i) a first chimeric gene selected from the group consisting of:

(a) a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-9 stearyl ACP desaturase ~~consisting essentially of~~ comprising the amino acid sequence set forth in SEQ ID NO:9, wherein all or part of the isolated nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-9 stearyl ACP desaturase, or the complement of ~~all or part of the fragment thereof~~, operably linked to at least one regulatory sequence ;

(b) a chimeric gene comprising (1) an isolated nucleic acid fragment encoding a corn delta-9 stearyl ACP desaturase ~~consisting essentially of~~ comprising the nucleotide sequence set forth in SEQ ID NO:9 wherein all or a part of the isolated nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-9 stearyl ACP desaturase, or the complement of ~~all or a part of the fragment thereof~~, and (2) an isolated nucleic acid fragment comprising a corn oleosin promoter ~~consisting essentially of~~ comprising the nucleotide sequence set forth in any of SEQ ID NOS: 38-40 and 42-49 wherein the isolated nucleic acid fragments of (1) and (2) are operably linked;

(c) a chimeric gene comprising (1) an isolated nucleic acid fragment encoding a corn delta-9 stearyl ACP desaturase ~~consisting essentially of~~ comprising the amino acid sequence set forth in SEQ ID NO:9 wherein all or part of the isolated nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-9 stearyl ACP or the complement of ~~all or part of the fragment thereof~~,

and 2) a shrunken 1 intron/exon, operably linked to at least one regulatory sequence, wherein the isolated nucleic acid fragments of (1) and (2) are operably linked; or

(d) a chimeric gene comprising (1) an isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase ~~consisting essentially of~~ comprising the amino acid sequence set forth in SEQ ID NO:9 wherein all or part of the isolated nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-9 stearoyl ACP desaturase, or the complement of ~~all or a part of the fragment thereof~~, (2) an isolated nucleic acid fragment comprising a corn oleosin promoter ~~consisting essentially of~~ comprising the nucleotide sequence set forth in any of SEQ ID NOS: 38-40 and 42-49, and (3) a shrunken 1 intron/exon wherein (1), (2) and (3) are operably linked, and

(ii) a second chimeric gene selected from the set consisting of:

(a) a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 90% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NO:1, wherein all or part of the isolated nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-12, or the complement of ~~all or a part of the fragment thereof~~, operably linked to at least one regulatory sequence;

(b) a chimeric gene comprising (1) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 90% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NO:1, wherein all or part of the isolated nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-12, or the complement of ~~all or a part of the fragment thereof~~, and (2) an isolated nucleic acid fragment comprising a corn oleosin promoter ~~consisting essentially of~~ comprising the nucleotide sequence set forth in any of SEQ ID NOS: 38-40 and 42-49 wherein the isolated nucleic acid fragments of (1) and (2) are operably linked;

(c) a chimeric gene comprising (1) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 90% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NO:1, wherein all or part of the

isolated nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-12 desaturase, or the complement of ~~all or a part of the~~ fragment thereof, and (2) a shrunken 1 intron/exon, operably linked to at least one regulatory sequence, wherein the isolated nucleic acid fragments of (1) and (2) are operably linked; or

(d) a chimeric gene comprising (1) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 90% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NO:1, wherein all or part of the isolated nucleic acid fragment is useful in co-suppressing an endogenous gene encoding a corn delta-12, or the complement of ~~all or a part of the fragment thereof~~, (2) an isolated nucleic acid fragment comprising a corn oleosin promoter ~~consisting essentially of comprising~~ the nucleotide sequence set forth in any of SEQ ID NOS: 38-40 and 42-49, and (3) a shrunken 1 intron/exon, wherein (1), (2) and (3) are operably linked; and further wherein expression of the chimeric genes results in an altered corn oil phenotype compared to the oil phenotype of a non transgenic corn grain.